



1600

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## RAW SEQUENCE LISTING

DATE: 06/04/2003

PATENT APPLICATION: US/09/829,936B

TIME: 15:49:40

Input Set : A:\ep.txt

Output Set: N:\CRF4\06042003\I829936B.raw

3 <110> APPLICANT: Conseiller, Emmanuel  
 4 Debussche, Laurent  
 5 Gallagher, William  
 7 <120> TITLE OF INVENTION: Polypeptide (MBP1) Capable Of Interacting With Oncogenic  
 Mutants Of The  
 8 P53 Protein  
 10 <130> FILE REFERENCE: ST98033  
 12 <140> CURRENT APPLICATION NUMBER: 09/829,936B  
 13 <141> CURRENT FILING DATE: 2001-04-11  
 15 <150> PRIOR APPLICATION NUMBER: FR9812754  
 16 <151> PRIOR FILING DATE: 1998-10-12  
 18 <160> NUMBER OF SEQ ID NOS: 33  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 23  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Artificial Sequence  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: Oligonucleotide 5'-1(p53)  
 30 <400> SEQUENCE: 1  
 31 agatctgtat ggaggagccg cag 23  
 34 <210> SEQ ID NO: 2  
 35 <211> LENGTH: 29  
 36 <212> TYPE: DNA  
 37 <213> ORGANISM: Artificial Sequence  
 39 <220> FEATURE:  
 40 <223> OTHER INFORMATION: Oligonucleotide 3' -393 (p53)  
 42 <400> SEQUENCE: 2  
 43 agatctcatc agtctgagtc aggcccttc 29  
 46 <210> SEQ ID NO: 3  
 47 <211> LENGTH: 15  
 48 <212> TYPE: DNA  
 49 <213> ORGANISM: Artificial Sequence  
 51 <220> FEATURE:  
 52 <223> OTHER INFORMATION: Oligonucleotide H175 3'  
 54 <400> SEQUENCE: 3  
 55 ggggcagtgc ctcac 15  
 58 <210> SEQ ID NO: 4  
 59 <211> LENGTH: 15  
 60 <212> TYPE: DNA  
 61 <213> ORGANISM: Artificial Sequence  
 63 <220> FEATURE:  
 64 <223> OTHER INFORMATION: Oligonucleotide W248 3'  
 66 <400> SEQUENCE: 4

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72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
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80 acaaacatgc acctc                                     15
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84 <211> LENGTH: 15
85 <212> TYPE: DNA
86 <213> ORGANISM: Artificial Sequence
88 <220> FEATURE:
89 <223> OTHER INFORMATION: Oligonucleotide G281 3'
91 <400> SEQUENCE: 6
92 gcgccgcct ctccc                                     15
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97 <212> TYPE: DNA
98 <213> ORGANISM: Artificial Sequence
100 <220> FEATURE:
101 <223> OTHER INFORMATION: Oligonucleotide 5'-73
103 <400> SEQUENCE: 7
104 agatctgtgt ggccccctgca cca                         23
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108 <211> LENGTH: 1021
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110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Murine MBP1 C-term fragment
115 <220> FEATURE:
116 <221> NAME/KEY: CDS
117 <222> LOCATION: (1)..(885)
119 <400> SEQUENCE: 8
120 tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg gac       48
121 Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
122 1          5          10          15
124 ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg       96
125 Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
126          20          25          30
128 ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct       144
129 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
130          35          40          45
132 aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca       192
133 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
134          50          55          60
136 tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt       240
137 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys

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138 65          70          75          80
140 aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc      288
141 Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
142          85          90          95
144 gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac      336
145 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
146          100          105          110
148 gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg      384
149 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
150          115          120          125
152 gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac      432
153 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
154          130          135          140
156 caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac cgc      480
157 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
158 145          150          155          160
160 tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac      528
161 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
162          165          170          175
164 aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag cct      576
165 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
166          180          185          190
168 tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg      624
169 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
170          195          200          205
172 cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt gcc      672
173 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
174          210          215          220
176 tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc tac      720
177 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
178 225          230          235          240
180 att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca      768
181 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
182          245          250          255
184 gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg      816
185 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
186          260          265          270
188 aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc      864
189 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
190          275          280          285
192 ttt gtg gga gcc tat acc ttc tgaagaccct caggggaagg ccatgtgggg      915
193 Phe Val Gly Ala Tyr Thr Phe
194          290          295
196 gccccttccc cctcccatag ctttaagcagc cccggggggcc tagggatgac cgttctgctt      975
198 aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa      1021
201 <210> SEQ ID NO: 9
202 <211> LENGTH: 295
203 <212> TYPE: PRT
204 <213> ORGANISM: Artificial Sequence

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206 <220> FEATURE:
207 <223> OTHER INFORMATION: Murine MBP1 C-term fragment
209 <400> SEQUENCE: 9
211 Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
212 1 5 10 15
215 Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
216 20 25 30
219 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
220 35 40 45
223 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
224 50 55 60
227 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
228 65 70 75 80
231 Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
232 85 90 95
235 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
236 100 105 110
239 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
240 115 120 125
243 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
244 130 135 140
247 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
248 145 150 155 160
251 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
252 165 170 175
255 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
256 180 185 190
259 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
260 195 200 205
263 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
264 210 215 220
267 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
268 225 230 235 240
271 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
272 245 250 255
275 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
276 260 265 270
279 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
280 275 280 285
283 Phe Val Gly Ala Tyr Thr Phe
284 290 295
287 <210> SEQ ID NO: 10
288 <211> LENGTH: 39
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Oligonucleotide c-myc 5'
295 <400> SEQUENCE: 10
296 gatccatgga gcagaagctg atctccgagg aggacctga

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Input Set : A:\ep.txt

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299 <210> SEQ ID NO: 11
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301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <223> OTHER INFORMATION: Oligonucleotide c-myc 3'
307 <400> SEQUENCE: 11
308 gatctcaggt cctcctcgga gatcagcttc tgctccatg          39
311 <210> SEQ ID NO: 12
312 <211> LENGTH: 45
313 <212> TYPE: DNA
314 <213> ORGANISM: Artificial Sequence
316 <220> FEATURE:
317 <223> OTHER INFORMATION: 5' MCS oligonucleotide
319 <400> SEQUENCE: 12
320 gatctcggtc gacctgcatg caattcccgg gtgcggccgc gagct          45
323 <210> SEQ ID NO: 13
324 <211> LENGTH: 37
325 <212> TYPE: DNA
326 <213> ORGANISM: Artificial Sequence
328 <220> FEATURE:
329 <223> OTHER INFORMATION: 3' MCS oligonucleotide
331 <400> SEQUENCE: 13
332 cgcggccgca cccgggaatt gcatgcaggt cgaccga          37
335 <210> SEQ ID NO: 14
336 <211> LENGTH: 22
337 <212> TYPE: DNA
338 <213> ORGANISM: Artificial Sequence
340 <220> FEATURE:
341 <223> OTHER INFORMATION: Oligonucleotide 3' mMBP1
343 <400> SEQUENCE: 14
344 cgggtactggc agaggtaact gg          22
347 <210> SEQ ID NO: 15
348 <211> LENGTH: 1513
349 <212> TYPE: DNA
350 <213> ORGANISM: Artificial Sequence
352 <220> FEATURE:
353 <223> OTHER INFORMATION: MBP1 murine (complete sequence)
355 <220> FEATURE:
356 <221> NAME/KEY: CDS
357 <222> LOCATION: (49)..(1377)
359 <400> SEQUENCE: 15
360 gctgtggcag aaaccctga cttctgccca ccacctccca gcctcagg atg ctc cct          57
361                                     Met Leu Pro
362                                     1
364 ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg          105
365 Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu
366   5               10               15
368 ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc          153

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**VERIFICATION SUMMARY**

DATE: 06/04/2003

PATENT APPLICATION: US/09/829,936B

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Input Set : A:\ep.txt

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